

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/681,878B
Source: IFW/b
Date Processed by STIC: 7/5/06

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 07/05/2006
PATENT APPLICATION: US/10/681,878B TIME: 14:22:51

Input Set : A:\44463336.APP
Output Set: N:\CRF4\07052006\J681878B.raw

3 <110> APPLICANT: CHIANG, VINCENT L.
 4 CARRAWAY, DANIEL T.
 5 SMELTZER, RICHARD H.
 7 <120> TITLE OF INVENTION: PRODUCTION OF SYRINGYL LIGNIN IN GYMNOSPERMS
 9 <130> FILE REFERENCE: 044463-0336
 11 <140> CURRENT APPLICATION NUMBER: 10/681,878B
 12 <141> CURRENT FILING DATE: 2003-10-09
 14 <150> PRIOR APPLICATION NUMBER: 09/796,256
 15 <151> PRIOR FILING DATE: 2001-02-28
 17 <150> PRIOR APPLICATION NUMBER: 08/991,677
 18 <151> PRIOR FILING DATE: 1997-12-16
 20 <150> PRIOR APPLICATION NUMBER: 60/033,381
 21 <151> PRIOR FILING DATE: 1996-12-16
 23 <160> NUMBER OF SEQ ID NOS: 24
 25 <170> SOFTWARE: PatentIn Ver. 3.3
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1708
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Liquidambar styraciflua
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (48)..(1571)
 36 <400> SEQUENCE: 1
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 38 Met Ala Phe
 39 1
 41 ctt cta ata ccc atc tca ata atc ttc atc gtc tta gct tac cag ctc 104
 42 Leu Leu Ile Pro Ile Ser Ile Ile Phe Ile Val Leu Ala Tyr Gln Leu
 43 5 10 15
 45 tat caa cgg ctc aga ttt aag ctc cca ccc ggc cca cgt cca tgg ccg 152
 46 Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg Pro Trp Pro
 47 20 25 30 35
 49 atc gtc gga aac ctt tac gac ata aaa ccg gtg agg ttc ccg tgt ttc 200
 50 Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe Arg Cys Phe
 51 40 45 50
 53 gcc gag tgg tca caa gcg tac ggt ccg atc ata tcg gtg tgg ttc ggt 248
 54 Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val Trp Phe Gly
 55 55 60 65
 57 tca acg ttg aat gtg atc gta tcg aat tcg gaa ttg gct aag gaa gtg 296
 58 Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala Lys Glu Val
 59 70 75 80
 61 ctc aag gaa aaa gat caa caa ttg gct gat agg cat agg agt aga tca 344
 62 Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg Ser Arg Ser

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63	85	90	95	
65	gct gcc aaa ttt agc agg gat ggg cag gac ctt ata tgg gct gat tat			392
66	Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp Ala Asp Tyr			
67	100	105	110	115
69	gga cct cac tat gtg aag gtt aca aag gtt tgt acc ctc gag ctt ttt			440
70	Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu Glu Leu Phe			
71	120	125	130	
73	act cca aag cgg ctt gaa gct ctt aga ccc att aga gaa gat gaa gtt			488
74	Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu Asp Glu Val			
75	135	140	145	
77	aca gcc atg gtt gag tcc att ttt aat gac act gcg aat cct gaa aat			536
78	Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn Pro Glu Asn			
79	150	155	160	
81	tat ggg aag agt atg ctg gtg aag aag tat ttg gga gca gta gca ttc			584
82	Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala Val Ala Phe			
83	165	170	175	
85	aac aac att aca aga ctc gca ttt gga aag cga ttc gtg aat tca gag			632
86	Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val Asn Ser Glu			
87	180	185	190	195
89	ggt gta atg gac gag caa gga ctt gaa ttt aag gaa att gtg gcc aat			680
90	Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile Val Ala Asn			
91	200	205	210	
93	gga ctc aag ctt ggt gcc tca ctt gca atg gct gag cac att cct tgg			728
94	Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His Ile Pro Trp			
95	215	220	225	
97	ctc cgt tgg atg ttc cca ctt gag gaa ggg gcc ttt gcc aag cat ggg			776
98	Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala Lys His Gly			
99	230	235	240	
101	gca cgt agg gac cga ctt acc aga gct atc atg gaa gag cac aca ata			824
102	Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu His Thr Ile			
103	245	250	255	
105	gcc cgt aaa aag agt ggt gga gcc caa caa cat ttc gtg gat gca ttg			872
106	Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val Asp Ala Leu			
107	260	265	270	275
109	ctc acc cta caa gag aaa tat gac ctt agc gag gac act att att ggg			920
110	Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr Ile Ile Gly			
111	280	285	290	
113	ctc ctt tgg gat atg atc act gca ggc atg gac aca acc gca atc tct			968
114	Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr Ala Ile Ser			
115	295	300	305	
117	gtc gaa tgg gcc atg gcc gag tta att aag aac cca agg gtc caa caa			1016
118	Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg Val Gln Gln			
119	310	315	320	
121	aaa gct caa gag gag cta gac aat gta ctt ggg tcc gaa cgt gtc ctg			1064
122	Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu Arg Val Leu			
123	325	330	335	
125	acc gaa ttg gac ttc tca agc ctc cct tat cta caa tgt gta gcc aag			1112
126	Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys Val Ala Lys			
127	340	345	350	355

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129	gag	gca	cta	agg	ctg	cac	cct	cca	aca	cca	cta	atg	ctc	cct	cat	cgc	1160		
130	Glu	Ala	Leu	Arg	Leu	His	Pro	Pro	Thr	Pro	Leu	Met	Leu	Pro	His	Arg			
131							360				365				370				
133	gcc	aat	gcc	aac	gtc	aaa	att	ggt	ggc	tac	gac	atc	cct	aag	gga	tca	1208		
134	Ala	Asn	Ala	Asn	Val	Lys	Ile	Gly	Gly	Tyr	Asp	Ile	Pro	Lys	Gly	Ser			
135							375				380			385					
137	aat	gtt	cat	gtt	aat	gtc	tgg	gcc	gtg	gtc	cgt	gat	cca	gca	gtg	tgg	1256		
138	Asn	Val	His	Val	Asn	Val	Trp	Ala	Val	Ala	Arg	Asp	Pro	Ala	Val	Trp			
139							390				395			400					
141	cgt	gac	cca	cta	gag	ttt	cga	ccg	gaa	cg	ttc	tct	gaa	gac	gat	gtc	1304		
142	Arg	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Ser	Glu	Asp	Asp	Val			
143							405				410			415					
145	gac	atg	aaa	gg	gt	cac	gat	tat	agg	cta	ctg	ccg	ttt	gg	gca	ggg	agg		
146	Asp	Met	Lys	Gly	His	Asp	Tyr	Arg	Leu	Leu	Pro	Phe	Gly	Ala	Gly	Arg			
147							420				425			430			435		
149	cgt	gtt	tgc	ccc	gg	gt	gca	caa	ctt	ggc	atc	aat	ttg	gtc	aca	tcc	atg		
150	Arg	Val	Cys	Pro	Gly	Ala	Gln	Leu	Gly	Ile	Asn	Leu	Val	Thr	Ser	Met			
151							440				445			450					
153	atg	gg	cac	cta	ttg	cac	cat	ttc	tat	tgg	agc	cct	cct	aaa	gg	gt	1448		
154	Met	Gly	His	Leu	Leu	His	His	Phe	Tyr	Trp	Ser	Pro	Pro	Lys	Gly	Val			
155							455				460			465					
157	aaa	cca	gag	gag	att	gac	atg	tca	gag	aat	cca	gga	ttg	gtc	acc	tac	1496		
158	Lys	Pro	Glu	Glu	Ile	Asp	Met	Ser	Glu	Asn	Pro	Gly	Leu	Val	Thr	Tyr			
159							470				475			480					
161	atg	cga	acc	ccg	gt	caa	gct	gtt	ccc	act	cca	agg	ctg	cct	gct	cac	1544		
162	Met	Arg	Thr	Pro	Val	Gln	Ala	Val	Pro	Thr	Pro	Arg	Leu	Pro	Ala	His			
163							485				490			495					
165	ttg	tac	aaa	cgt	gt	gt	gct	gt	atg	taattcttag	tttgttatta						1591		
166	Leu	Tyr	Lys	Arg	Val	Ala	Val	Asp	Met										
167	500						505												
169	ttc	atg	ct	ta	agg	ttt	tg	gac	ttt	gaa	tt	at	gt	aaaa	tt	cca	agt	ga	1651
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175	<211>	LENGTH:	508																
176	<212>	TYPE:	PRT																
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183	Tyr	Gln	Leu	Tyr	Gln	Arg	Leu	Arg	Phe	Lys	Leu	Pro	Pro	Gly	Pro	Arg			
184							20				25			30					
186	Pro	Trp	Pro	Ile	Val	Gly	Asn	Leu	Tyr	Asp	Ile	Lys	Pro	Val	Arg	Phe			
187							35				40			45					
189	Arg	Cys	Phe	Ala	Glu	Trp	Ser	Gln	Ala	Tyr	Gly	Pro	Ile	Ile	Ser	Val			
190							50				55			60					
192	Trp	Phe	Gly	Ser	Thr	Leu	Asn	Val	Ile	Val	Ser	Asn	Ser	Glu	Leu	Ala			
193							65				70			75			80		
195	Lys	Glu	Val	Leu	Lys	Glu	Lys	Asp	Gln	Gln	Leu	Ala	Asp	Arg	His	Arg			
196							85				90			95					

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198 Ser Arg Ser Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp
 199 100 105 110
 201 Ala Asp Tyr Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu
 202 115 120 125
 204 Glu Leu Phe Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu
 205 130 135 140
 207 Asp Glu Val Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn
 208 145 150 155 160
 210 Pro Glu Asn Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala
 211 165 170 175
 213 Val Ala Phe Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val
 214 180 185 190
 216 Asn Ser Glu Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile
 217 195 200 205
 219 Val Ala Asn Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His
 220 210 215 220
 222 Ile Pro Trp Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala
 223 225 230 235 240
 225 Lys His Gly Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu
 226 245 250 255
 228 His Thr Ile Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val
 229 260 265 270
 231 Asp Ala Leu Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr
 232 275 280 285
 234 Ile Ile Gly Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr
 235 290 295 300
 237 Ala Ile Ser Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg
 238 305 310 315 320
 240 Val Gln Gln Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu
 241 325 330 335
 243 Arg Val Leu Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys
 244 340 345 350
 246 Val Ala Lys Glu Ala Leu Arg Leu His Pro Pro Thr Pro Leu Met Leu
 247 355 360 365
 249 Pro His Arg Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro
 250 370 375 380
 252 Lys Gly Ser Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro
 253 385 390 395 400
 255 Ala Val Trp Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu
 256 405 410 415
 258 Asp Asp Val Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly
 259 420 425 430
 261 Ala Gly Arg Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val
 262 435 440 445
 264 Thr Ser Met Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro
 265 450 455 460
 267 Lys Gly Val Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu
 268 465 470 475 480
 270 Val Thr Tyr Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu

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271	485	490	495
273	Pro Ala His Leu Tyr Lys Arg Val Ala Val Asp Met		
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284	<221> NAME/KEY: CDS		
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291	Met Asp Ser Ser Leu His Glu Ala Leu Gln Pro Leu		
292	1 5 10		
294	ccc atg acg ctg ttc att ata cct ttg cta ctc tta ttg ggc cta	157	
295	Pro Met Thr Leu Phe Phe Ile Ile Pro Leu Leu Leu Leu Gly Leu		
296	15 20 25		
298	gta tct cgg ctt cgc cag aga cta cca tac cca cca ggc cca aaa ggc	205	
299	Val Ser Arg Leu Arg Gln Arg Leu Pro Tyr Pro Pro Gly Pro Lys Gly		
300	30 35 40		
302	tta ccg gtg atc gga aac atg ctc atg atg gat caa ctc act cac cga	253	
303	Leu Pro Val Ile Gly Asn Met Leu Met Asp Gln Leu Thr His Arg		
304	45 50 55 60		
306	gga ctc gcc aaa ctc gcc aaa caa tac ggc ggt cta ttc cac ctc aag	301	
307	Gly Leu Ala Lys Leu Ala Lys Gln Tyr Gly Gly Leu Phe His Leu Lys		
308	65 70 75		
310	atg gga ttc tta cac atg gtg gcc gtt tcc aca ccc gac atg gct cgc	349	
311	Met Gly Phe Leu His Met Val Ala Val Ser Thr Pro Asp Met Ala Arg		
312	80 85 90		
314	caa gtc ctt caa gtc caa gac aac atc ttc tcg aac cgg cca gcc acc	397	
315	Gln Val Leu Gln Val Gln Asp Asn Ile Phe Ser Asn Arg Pro Ala Thr		
316	95 100 105		
318	ata gcc atc agc tac ctc acc tat gac cga gcc gac atg gcc ttc gct	445	
319	Ile Ala Ile Ser Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala		
320	110 115 120		
322	cac tac ggc ccg ttt tgg cgt cag atg cgt aaa ctc tgc gtc atg aaa	493	
323	His Tyr Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys		
324	125 130 135 140		
326	tta ttt agc cgg aaa cga gcc gag tcg tgg gag tcg gtc cga gac gag	541	
327	Leu Phe Ser Arg Lys Arg Ala Glu Ser Trp Glu Ser Val Arg Asp Glu		
328	145 150 155		
330	gtc gac tcg gca gta cga gtg gtc gcg tcc aat att ggg tcg acg gtg	589	
331	Val Asp Ser Ala Val Arg Val Val Ala Ser Asn Ile Gly Ser Thr Val		
332	160 165 170		
334	aat atc ggc gag ctg gtt ttt gct ctg acg aag aat att act tac agg	637	
335	Asn Ile Gly Glu Leu Val Phe Ala Leu Thr Lys Asn Ile Thr Tyr Arg		
336	175 180 185		
338	gcg gct ttt ggg acg atc tcg cat gag gac cag gag ttc gtg gcc	685	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; Xaa Pos. 3,5,6,8

Seq#:22; N Pos. 23

VERIFICATION SUMMARY

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L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0

L:1278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0